



Sequence listing

<110> Kaneka Corporation

<120> Process for producing coenzyme Q10

<130> T549/QX-GT2

<150> JP P1999-237581

<151> 1999-08-24

<160> 2 8

<210> 1

<211> 1653

<212> DNA

<213> Saioella complicata

<400> 1

ttttgtgggg tcgaaaagtc ggcacgggtg cagggttcggc ttgagaccag taaaggctcg 60

gagattgagt tcaggacaaa gctttgatcc gtgaggtcta catcttcagc aaatcatttc 120

aaatccatat acc atg gcc tca cca gca ctg cgg ata cga agc atc agc 169
Met Ala Ser Pro Ala Leu Arg Ile Arg Ser Ile Ser
1 5 10

tct cga tca atc gcc tct ctg cga tgg gtt acc cta aga aca gcc tcg 217
Ser Arg Ser Ile Ala Ser Leu Arg Ser Val Thr Leu Arg Thr Ala Ser
15 20 25

gca cct tca tta cga cta aga tgt acc cgg acg ago cgg cca tcg agt 265
Ala Pro Ser Leu Arg Leu Arg Cys Thr Pro Thr Ser Arg Pro Ser Ser
30 35 40

tca tgg get get get gtg tct tcg gcg tcg aga ctg gtt gag cct gat 313
Ser Trp Ala Ala Ala Val Ser Ser Ala Ser Arg Leu Val Glu Pro Asp
45 50 55 60

ccg aat caa cct ctc atc aat ccg ctc aac ttg gtc ggt ccc gag atg 361
Pro Asn Gln Pro Leu Ile Asn Pro Leu Asn Leu Val Gly Pro Glu Met
65 70 75

tca aat ctt aca tcc aac atc cga tct ctc ctc ggt tca gga cac cct 409
Ser Asn Leu Thr Ser Asn Ile Arg Ser Leu Leu Gly Ser Gly His Pro
80 85 90

tct ctc gac act gtc get aaa tac tat gtt cag tct gag gga aag cat 457
Ser Leu Asp Thr Val Ala Lys Tyr Tyr Val Gln Ser Glu Gly Lys His
95 100 105

att cgt cgg ctc atg gta ctg ctg atg get cag gcg acg gag gtt gcg 505
Ile Arg Pro Leu Met Val Leu Leu Met Ala Gln Ala Thr Glu Val Ala
110 115 120

cca aaa gtt cag ggt tgg gag aag gtc gtg gag gtt ccg gtc aac gag 553
Pro Lys Val Gln Gly Trp Glu Lys Val Val Glu Val Pro Val Asn Glu
125 130 135 140

gga ctc gca cca cca gag gtg ctc aat gac aag aac cca gat atg atg	601
Gly Leu Ala Pro Pro Glu Val Leu Asn Asp Lys Asn Pro Asp Met Met	
145 150 155	
aac atg agg tca gga cca tta acg aag gac ggc gag atc gag gga cag	649
Asn Met Arg Ser Gly Pro Leu Thr Lys Asp Gly Glu Ile Glu Gly Gln	
160 165 170	
acg tcg aat atc ctc gcc tcg caa cgg cgg ttg get gag atc acg gag	697
Thr Ser Asn Ile Leu Ala Ser Gln Arg Arg Leu Ala Glu Ile Thr Glu	
175 180 185	
atg atc cat gca gca tca ctc ctc cac gac gac gtt atc gac get tcc	745
Met Ile His Ala Ala Ser Leu Leu His Asp Asp Val Ile Asp Ala Ser	
190 195 200	
gag acc aga cga aac gca cca tcc gga aac cag gca ttc gga aac aag	793
Glu Thr Arg Arg Asn Ala Pro Ser Gly Asn Gln Ala Phe Gly Asn Lys	
205 210 215 220	
atg gcg att ttg get ggt gat ttc ttg ttg gga cgg gcg tct gtt gca	841
Met Ala Ile Leu Ala Gly Asp Phe Leu Leu Gly Arg Ala Ser Val Ala	
225 230 235	
67 ttg gcg agg ttg cgc aat ccg gag gtg att gag ctt ttg get act gtt	889
Leu Ala Arg Leu Arg Asn Pro Glu Val Ile Glu Leu Leu Ala Thr Val	
240 245 250	
att gca aac ttg gtt gag gga gag ttc atg cag ttg aaa aat act gtt	937
Ile Ala Asn Leu Val Glu Gly Glu Phe Met Gln Leu Lys Asn Thr Val	
255 260 265	
gat gat gcg att gag get acg gcg acg cag gaa acg ttc gat tac tat	985
Asp Asp Ala Ile Glu Ala Thr Ala Thr Gln Glu Thr Phe Asp Tyr Tyr	
270 275 280	
ttg cag aag act tac ttg aag act gcg tcc ttg att gcc aag tcg tgc	1033
Leu Gln Lys Thr Tyr Leu Lys Thr Ala Ser Leu Ile Ala Lys Ser Cys	
285 290 295 300	
aga gca agt gcg ctt etg ggt ggt get acg ect gag gtt get gat get	1081
Arg Ala Ser Ala Leu Leu Gly Gly Ala Thr Pro Glu Val Ala Asp Ala	
305 310 315	
gct tat gct tac gga agg aac ctt ggt ttg gca ttc cag atc gtc gac	1129
Ala Tyr Ala Tyr Gly Arg Asn Leu Gly Leu Ala Phe Gln Ile Val Asp	
320 325 330	
gac atg ctc gac tac acc gtc tcc get acc gac ctc ggt aag ccc gcc	1177
Asp Met Leu Asp Tyr Thr Val Ser Ala Thr Asp Leu Gly Lys Pro Ala	
335 340 345	
ggt gca gac ctc cag ctc ggt ctc gcc acc gcg ccg gcc ctc ttc gca	1225
Gly Ala Asp Leu Gln Leu Gly Leu Ala Thr Ala Pro Ala Leu Phe Ala	
350 355 360	
tgg aag cac cac gcc gag ctc ggt ccc atg atc aag cgc aag ttc tct	1273
Trp Lys His His Ala Glu Leu Gly Pro Met Ile Lys Arg Lys Phe Ser	
365 370 375 380	

gac cca gga gac gtc gag cgt gca cgc gag ttg gtc gag aaa agt gat 1321
Asp Pro Gly Asp Val Glu Arg Ala Arg Glu Leu Val Glu Lys Ser Asp
385 390 395

gga ttg gag aag acg aga gcc ttg gcg gag gag tat gcc cag aag gcg 1369
Gly Leu Glu Lys Thr Arg Ala Leu Ala Glu Glu Tyr Ala Gln Lys Ala
400 405 410

ttg gat gca att cgg acg ttc ccg gag agt cog gca cgg aag get ttg 1417
Leu Asp Ala Ile Arg Thr Phe Pro Glu Ser Pro Ala Arg Lys Ala Leu
415 420 425

gag cag ttg acg gac aag gtg ttg act agg tca aga taggaattcgagct 1467
Glu Gln Leu Thr Asp Lys Val Leu Thr Arg Ser Arg
430 435 440

cggtagcccg ggatcctcta gagtcgacct gcaggcatgc aagcttggt gttttggcgg 1527
atgagagaag attttcagcc tgatacagat taaatcagaa cgcagaagcg gtctgataaa 1587
acagaatttg cctggcgga gtagcgcggt ggtccacact gaccccatgc cgaactcaga 1647
agtgaa 1653

<210> 2
<211> 440
<212> PRT
<213> Saioella complicata

<400> 2
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Ile Ala Ser Leu Arg Ser Val Thr Leu Arg Thr Ala Ser Ala Pro
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Ser Leu Arg Leu Arg Cys Thr Pro Thr Ser Arg Pro Ser Ser Ser
35 40 45
Trp Ala Ala Ala Val Ser Ser Ala Ser Arg Leu Val Glu Pro Asp
50 55 60
Pro Asn Gln Pro Leu Ile Asn Pro Leu Asn Leu Val Gly Pro Glu
65 70 75
Met Ser Asn Leu Thr Ser Asn Ile Arg Ser Leu Leu Gly Ser Gly
80 85 90
His Pro Ser Leu Asp Thr Val Ala Lys Tyr Tyr Val Gln Ser Glu
95 100 105
Gly Lys His Ile Arg Pro Leu Met Val Leu Leu Met Ala Gln Ala
110 115 120
Thr Glu Val Ala Pro Lys Val Gln Gly Trp Glu Lys Val Val Glu
125 130 135
Val Pro Val Asn Glu Gly Leu Ala Pro Pro Glu Val Leu Asn Asp
140 145 150
Lys Asn Pro Asp Met Met Asn Met Arg Ser Gly Pro Leu Thr Lys
155 160 165
Asp Gly Glu Ile Glu Gly Gln Thr Ser Asn Ile Leu Ala Ser Gln
170 175 180
Arg Arg Leu Ala Glu Ile Thr Glu Met Ile His Ala Ala Ser Leu
185 190 195
Leu His Asp Asp Val Ile Asp Ala Ser Glu Thr Arg Arg Asn Ala
200 205 210
Pro Ser Gly Asn Gln Ala Phe Gly Asn Lys Met Ala Ile Leu Ala
215 220 225

Gly Asp Phe Leu Leu Gly Arg Ala Ser Val Ala Leu Ala Arg Leu
 230 235 240
 Arg Asn Pro Glu Val Ile Glu Leu Leu Ala Thr Val Ile Ala Asn
 245 250 255
 Leu Val Glu Gly Glu Phe Met Gin Leu Lys Asn Thr Val Asp Asp
 260 265 270
 Ala Ile Glu Ala Thr Ala Thr Gin Glu Thr Phe Asp Tyr Tyr Leu
 275 280 285
 Gln Lys Thr Tyr Leu Lys Thr Ala Ser Leu Ile Ala Lys Ser Cys
 290 295 300
 Arg Ala Ser Ala Leu Leu Gly Gly Ala Thr Pro Glu Val Ala Asp
 305 310 315
 Ala Ala Tyr Ala Tyr Gly Arg Asn Leu Gly Leu Ala Phe Gin Ile
 320 325 330
 Val Asp Asp Met Leu Asp Tyr Thr Val Ser Ala Thr Asp Leu Gly
 335 340 345
 Lys Pro Ala Gly Ala Asp Leu Gin Leu Gly Leu Ala Thr Ala Pro
 350 355 360
 Ala Leu Phe Ala Trp Lys His His Ala Glu Leu Gly Pro Met Ile
 365 370 375
 Lys Arg Lys Phe Ser Asp Pro Gly Asp Val Glu Arg Ala Arg Glu
 380 385 390
 Leu Val Glu Lys Ser Asp Gly Leu Glu Lys Thr Arg Ala Leu Ala
 395 400 405
 Glu Glu Tyr Ala Gln Lys Ala Leu Asp Ala Ile Arg Thr Phe Pro
 410 415 420
 Glu Ser Pro Ala Arg Lys Ala Leu Glu Gln Leu Thr Asp Lys Val
 425 430 435
 Leu Thr Arg Ser Arg
 440

<210> 3

<211> 24

<212> DNA

<213> Artificial Sequence

<400> 3

aaggatcctn ytncaaygayg aygt 24

<210> 4

<211> 17

<212> DNA

<213> Artificial Sequence

<400> 4

arytgnadra aytcncc 17

<210> 5

<211> 21

<212> DNA

<213> Artificial Sequence

<400> 5

gagaccagac gaaacgcacc a 21

<210> 6

<211> 21

<212> DNA

<213> Artificial Sequence

<400> 6

tggtgcgttt cgtctggtct c 21

<210> 7

<211> 26

<212> DNA

<213> Artificial Sequence

<400> 7

aacatatggc ctcaccagca ctgcgg 26

<210> 8

<211> 29

<212> DNA

<213> Artificial Sequence

<400> 8

aagaattcct atcttgacct agtcaacac 29